

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 09:20:45 : Search time 48 Seconds
(without alignments)
5513.793 Million cell updates/sec

Title: US-10-021-811-35
Perfect score: 863
Sequence: 1 gcacgagctctatcacacac.....aaaaaaaaaaaaaaaaaaaa 863

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: February 18, 2003, 10:32:30
Job time : 48 secs

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 09:21:50 ; Search time 59 Seconds
(without alignments)
7449.937 Million cell updates/sec

Title: US-10-021-811-35
Perfect score: 863
Sequence: 1 gcacgagctctatcacac.....aaaaaaaaaaaaaaaaa 863

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 424239 seqs, 254661826 residues

Word size : 60

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PublishedApplications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	863	100.0	863	9	US-10-021-811-35
					Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-10-021-811-35
; Sequence 35, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Faug, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: B01294 US NA
; CURRENT APPLICATION NUMBER: US/10/021.811
; CURRENT FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Glycine max
US-10-021-811-35
Query Match 100.0%; Score 863; DB 9; Length 863;
Best Local Similarity 100.0%; Pred. No. 4.6e-301;
Matches 863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGAGCTCTATCACACACACAAAGTCAATGGATATAAAAAACAACAGTGTAAAGCTCTCA 60
DB 1 GCAGAGCTCTATCACACACACAAAGTCAATGGATATAAAAAACAACAGTGTAAAGCTCTCA 60
QY 61 AGATCCTGAAGTGAGAAAAGGGCTTGGACAATGGAAGAAGACTTGTATCTTGTGAACTA 120
DB 61 AGATCCTGAAGTGAGAAAAGGGCTTGGACAATGGAAGAAGACTTGTATCTTGTGAACTA 120
QY 121 TATTGCAAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAAACG 180
DB 121 TATTGCAAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAAACG 180
QY 181 TAACGAAAGAGTTCGCGCTAAGGTGGCTAAATTTACCTCCGCTCCTGATGTTAGAAAGAGG 240
DB 181 TAACGAAAGAGTTCGCGCTAAGGTGGCTAAGTGGCTTAATTTACCTCCGCTCCTGATGTTAGAAAGAGG 240
QY 241 GAATATTACACCCGAGGAAACAACCTTTTGTATTTGAGTCTCCAGCAAGTGGGGAACAG 300
DB 241 GAATATTACACCCGAGGAAACAACCTTTTGTATTTGAGTCTCCAGCAAGTGGGGAACAG 300
QY 301 GTGTCCTCAAAATGCCAAGCATCTACCTGGAAGACTGTAATGAGATCAAGAACTATTG 360
DB 301 GTGTCCTCAAAATGCCAAGCATCTACCTGGAAGACTGTAATGAGATCAAGAACTATTG 360
QY 361 GAGACAAGAGTCCAGAAAGCACATCAAGCAAGCTGAGAAGCTTTTCAGCAACAGAGTAGTAA 420
DB 361 GAGACAAGAGTCCAGAAAGCACATCAAGCAAGCTGAGAAGCTTTTCAGCAACAGAGTAGTAA 420
QY 421 TAATTCGAGATAAATGATCACCAGCTAGCACTAGCCATGTTTCCACCAGCTGAGCC 480
DB 421 TAATTCGAGATAAATGATCACCAGCTAGCACTAGCCATGTTTCCACCAGCTGAGCC 480
QY 481 CATGGAGATGTTTCTCCACCTGTTATCAAGAACTGTTAGAGCCATTTTCAACTCAGTT 540
DB 481 CATGGAGATGTTTCTCCACCTGTTATCAAGAACTGTTAGAGCCATTTTCAACTCAGTT 540
QY 541 CCTACAATTAATCCTGATCAATCCAGTTGTTGTACCAATGACAACAAACATTAACATA 600
DB 541 CCTACAATTAATCCTGATCAATCCAGTTGTTGTACCAATGACAACAAACATTAACATA 600
QY 601 TTGAGCATGGAGATAGCTGGTCAATGCAATTTACTGAACGGTGATTAATATATTAATCAAG 660
DB 601 TTGAGCATGGAGATAGCTGGTCAATGCAATTTACTGAACGGTGATTAATATATTAATCAAG 660
QY 661 ATAAACCTTAAGTTCATGAACTCCATAAGGCTGGAATGCTTGTGGATTAAACATATTAT 720
DB 661 ATAAACCTTAAGTTCATGAACTCCATAAGGCTGGAATGCTTGTGGATTAAACATATTAT 720
QY 721 TGGGTTTGTATATAGTAGTGGATGTTGGTGTTCGCTAGCATTATTAGTATGTGTC 780
DB 721 TGGGTTTGTATATAGTAGTGGATGTTGGTGTTCGCTAGCATTATTAGTATGTGTC 780
QY 781 TGAATATATACGAGATYTTATTAACATATATCGCATGCTTTATATATAAAAAAAA 840
DB 781 TGAATATATACGAGATYTTATTAACATATATCGCATGCTTTATATATAAAAAAAA 840
QY 841 AAAAAAAAAAAAAAAAAAAAAA 863
DB 841 AAAAAAAAAAAAAAAAAAAAAA 863

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 08:51:00 ; Search time 2196 Seconds
(without alignments)
11437.032 Million cell updates/sec

Title: US-10-021-811-35

Perfect score: 863

Sequence: 1 gcacgagctctatcacacac.....aaaaaaaaaaaaaaaaaaaa 863

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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No matches found

Search completed: February 18, 2003, 10:02:37
Job time : 2196 secs

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 08:14:20 ; Search time 220 Seconds
(without alignments)
8833.975 Million cell updates/sec

Title: US-10-021-811-35
Perfect score: 863
Sequence: 1 gcacgagctctatcacacac.....aaaaaaaaaaaaaaaaaaaa 863

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: February 18, 2003, 09:25:40
Job time : 221 secs

